

Please replace Table 2K on page 35 with the following:

Table 2K. Domain Analysis of NOV2			
<p>gnl Smart smart00110, C1q, Complement component C1q domain.; Globular domain found in many collagens and eponymously in complement C1q. When part of full length proteins these domains form a 'bouquet' due to the multimerization of heterotrimers. The C1q fold is similar to that of tumour necrosis factor.</p> <p>CD-Length = 132 residues, 84.1% aligned Score = 86.7 bits (213), Expect = 1e-18</p>			
Query:	91	MAVTFDKVYVNIGGDFDAAAGVFRCLPGAYFFSFTLGKLPKRTLSVKLMKNRDEVQAMI	
	150		
		V FDKV N G +D + G F C +PG Y+FS+ + + + + V LMKN +V	
Sbjct:	20	QPVRFDKVLYNQQGHYDPSTGKFTCPVPGVYYFSYHI-ESKGRNVKVS LMKNGIQVMRE-	77
Query:	151	YDDGASRRREMQSQSVM LALRRGDAVWLLSHDHDGYGAYS NHGKYITFSGFLVY	204
		D+ ++ S +L LR+GD VW L D G Y+ TFSGFL++	
Sbjct:	78	CDEYQKGLYQVASGGALLQLRQGDQVW-LELDDKKNGLYAGEEVDSTFSGFLLF	130 (SEQ
ID NO:	182)		

Please replace Table 3E on page 45 with the following:

Table 3E Domain Analysis of NOV3

gnl|Smart|smart00220, S_TKc, Serine/Threonine protein kinases, catalytic domain;
Phosphotransferases. Serine or threonine-specific kinase subfamily.

CD-Length = 256 residues, 100.0% aligned
Score = 237 bits (605), Expect = 1e-63

Query:	191	FSVHRIIGRGGFGEVYGCRKRD	TGKMYAMKCLDKKRIKMKQGETLALNERIMLSLVSTGD	250
		+ + ++G+G FG+VY R + TGK+ A+K + K+++K K+ E L E +L + D		
Sbjct:	1	YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKLKKKKRER-ILREIKILKKL---		56
Query:	251	CPFIVCMSYAFHTPDKLSFILDLMNGGDLHYHLSQHGVFSEADMRFYAAEIIILGLEHMHN		310
		P IV + F DKL +++ GGD L + G SE + RFYA +I+ LE++H+		
Sbjct:	57	HPNIVKLYDVFEDDDKLYLVMYCEGGDLFDLLKKRGRlseDEARFYARQILSALEYLHS		116
Query:	311	RFVVYRDLKPANILLDEHGHVRISDLGLACDFSKKKPHAS--VGTHGYMAPEVLQKGVAY		368
		+ +++RDLKP NILLD GHV+++D GLA + VGT YMAPEVL G Y		
Sbjct:	117	QGIIHRDLKPENILLDSGHVKLADFGLAQLDSSGGTLLTTFVGTPEYMAPEVL-LGKGY		175
Query:	369	DSSADWFSLGCMFLKLLRGHSPFRQHKTCDK-HEIDRMTLTMAVELPDSFSPELHSLLEG		427
		+ D +SLG +L++LL G PF + SPE L++		
Sbjct:	176	GKAVDIWSLGVILYELLTGKPPFPDQLLALFKKIGKPPPPFPPPEWKISPEAKDLIKK		235
Query:	428	LLQRDVNRRLGCLGRGAQEVKESPFF	453	
		LL +D +RL A+E E PFF		
Sbjct:	236	LLVKDPEKRL-----TAEAELEHPFF	256 (SEQ ID NO: 183)	

Please delete the paragraph following Table 3E on page 45.

Please replace Table 4E on page 63 with the following:

Table 4E. Domain Analysis of NOV4	
<p>gnl Pfam pfam01500, Keratin_B2, Keratin, high sulfur B2 protein. High sulfur proteins are cysteine-rich proteins synthesized during the differentiation of hair matrix cells, and form hair fibers in association with hair keratin intermediate filaments. This family has been divided up into four regions, with the second region containing 8 copies of a short repeat. This family is also known as B2 or KAP1.</p>	
<p>CD-Length = 144 residues, 87.5% aligned Score = 38.9 bits (89), Expect = 0.004</p>	
Query: 630	CIDVACSNHGTCTGTCTCICNPGYKGESCEEVDCMDPTCSGRGVCVRGECHCFVGWGGTNC
689	
Sbjct: 5	C CS GTC + C + SC + C P CS C R C + C
57	CGFPTCSTLGTGSSCC-----QPPSCCQPSCCQPVCSQTTCC-RPTCFQSSCCRPSCC
Query: 690	ETP--RATCLDQCSGHGTFLPDTGLCSCDPSWTGHDCSIEICAADCGGHGVCVGGTCRCE
747	
Sbjct: 58	+T + TC S G+ SC W DC +E
93	QTSCCQPTCCQSSSCQ----TGCGIGSCRTRWCRPDCRVE-----
Query: 748	DGWMGAACDQRACHPRCAEHGTCRDGKCECS---PGWNGEHC 786
	C C C C+ + S P + G+ C
Sbjct: 94	-----GTCLPPCCVVSCPTPTCCQPVSAQASCCRPSYCGQSC 130 (SEQ ID NO:
184)	

Please replace Table 6G on pages 84-85 with the following:

Table 6G. Domain Analysis of NOV6				
<p><u>gnl Pfam pfam01404</u>, EPH_lbd, Ephrin receptor ligand binding domain. The Eph receptors, which bind to ephrins pfam00812 are a large family of receptor tyrosine kinases. This family represents the amino terminal domain which binds the ephrin ligand.</p> <p>CD-Length = 174 residues, 100.0% aligned</p> <p>Score = 345 bits (886), Expect = 6e-96</p>				
Query:	33	QVLLDTSTVMGELGWKTYPLNGWDAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWIS	92	
		+V LLDLT+T GELGW TYP GW+ ++ +DE+NRPI TYQVCNVMEPNQNNWLRTNWI		
Sbjct:	1	EVTLLDTTTATGELGWLTYPPGGWEEVSGLDENNRPIRTYQVCNVMEPNQNNWLRTNWIP	60	
		o o o o o o		
Query:	93	RDAAQKIYVEMKFTLRDCNSIPWVLGTCKETF TLYYIESDESHGTFKFKPSQYIKIDTIAA	152	
		R AQ++YVE+KFT+RDCNS+P VLGTCKETF LYY ESDE G ++ +QY K+DTIAA		
Sbjct:	61	RRGAQRVYVELKFTVRDCNSLPGVLGTCKETFNLYYYEDEDVGPWRENQYTKVDTIAA	120	
Query:	153	DESFTQMDLGDRILKLNTEIREVGPIERKGFYLAQFDIGACIALVSVRVFYKKC	206	
		DESFTQ+DLGDR++KLNTE+R VGP+ +KGFYLAQFD+GAC+ALVSVRVFYKKC		
Sbjct:	121	DESFTQVDLGDRVMKLNTEVRSVGPLSKKGFYLAQFDVGACMALVSVRVFYKKC	174 (SEQ	
ID NO:	185)			

Please replace Table 7E on pages 92-93 with the following:

Table 7E. Domain Analysis of NOV7				
gnl Pfam pfam00083, sugar_tr, Sugar (and other) transporter.				
CD-Length = 447 residues, 96.6% aligned				
Score = 246 bits (629), Expect = 2e-66				
Query:	21	FQVFKSFYNETYFERHATFM----DGKLMLLWSCTVSMFPLGGLLGSLLVGLLVDS	76	
		V F F + +L VS+F +G +GSL G L D GR		
Sbjct:	16	TGVIGGFATLIDFLFFFGGLTSSGSCAESTVLSGLVVSIFVGRPIGSLFAGKLGDRFGR	75	
Query:	77	KGTLLINNIFAIIPAILMGVSKVAKAFELIVFSRVVLGVCAGISYSALPMYLGELAPKNL	136	
		K +LLI + +I ++L G++ A F L++ RV++G+ G + +PMY+ E+APK L		
Sbjct:	76	KKSLLIGLVLFVIGSLLSGLAPGA--FYLLIVGRVLVGLGVGGASVLVPMYISEIAPKAL	133	
Query:	137	RGMVGTMTVEFVIVGVFLAQIFSLQAILGNPAGWPVLLALTGVPALLQLLTLPFFPESPR	196	
		RG +G++ ++ + +G+ +A I L N GW + L L VPALL L+ L F PESPR		
Sbjct:	134	RGALGSLYQLGITIGILVAAIIGLGLNKTNNWGWRIPLGLQLVPALLLLIGLLFLPESPR	193	
Query:	197	YSLIQKGDEATARPLRRLRGHTDMEAELEDMAEARAERAEGHLSVLHLCALRSRQWLL	256	
		+ +++ E L +LRG D++ E+++ +AE A + + R +LL		
Sbjct:	194	WLVLGKLEEARAVLAKLRGVEDVDQEIQEEKAELEAGVSSEKAGLELF--RGRTRQRLL	251	
Query:	257	SIIVLMAGQQLSGINAINYYADTIYTSAGVEAAHSQYVTVGSGVVNI VMTITSVVLVERL	316	
		++L QQL+GINAI YY+ TI+ S G+ + + VT+ GVVN V T ++ LV+R		
Sbjct:	252	MGVMLQIFQQLTGINAI FYYSPTIFKSVGMSD VALLVTIIVGVVNFVATFVAIFLVDRF	311	
Query:	317	GRRHLLLAGYGICGSACLVLTVSPPPPQNRVPELSYLGII CVFAYIAGHSIGPSPVPSVVR	376	
		GRR LLL G L+L V+ P + I+ + +IA ++G P+P V+		
Sbjct:	312	GRRPLLLLGAAGMAICFLILGVA-LLLLNKPGAGIVAIVFILLFIAFFALGWGPIPVIL	370	
Query:	377	TEIFLQSSRRRAAFMVDGAVHWLNTNFIIGFLFPISIQEAIG-AYSFII FAGICLLTAIYIYV	435	
		+E+F R A + A +WL NFIIGFLFP I AIG Y F+ FAG+ +L +++Y		
Sbjct:	371	SELFPTGVRSKAMALATAANWLANFIIGFLFPYITGAIGGGYVFLFFAGLLVLFILFVYF	430	
Query:	436	VIPETKGKTFVEINRIF 452		
		+PETKG+T EI+ +F		
Sbjct:	431	FVPETKGRTLEEIDELF 447 (SEQ ID NO: 186)		

Please replace Table 8E on page 101 with the following:

Table 8E. Domain Analysis of NOV8			
<u>gnl Smart smart00179</u> , EGF_CA, Calcium-binding EGF-like domain			
CD-Length = 41 residues, 80.5% aligned			
Score = 52.8 bits (125), Expect = 7e-08			
Query:	125	DIDECEVSGLCRHGGRCVNTHGSFECY-CMDGY	156
		DIDEC C++GG CVNT GS+ C C GY	
Sbjct:	1	DIDECASGNPCQNGGTCVNTVGSYRCEECPPGY	33 (SEQ ID NO: 187)

Please replace Table 9E on page 109 with the following:

Table 9E. Domain Analysis of NOV9			
<u>gnl Smart smart00179</u> , EGF_CA, Calcium-binding EGF-like domain			
CD-Length = 41 residues, 80.5% aligned			
Score = 52.8 bits (125), Expect = 7e-08			
Query:	125	DIDECEVSGLCRHGGRCVNTHGSFECY-CMDGY	156
		DIDEC C++GG CVNT GS+ C C GY	
Sbjct:	1	DIDECASGNPCQNGGTCVNTVGSYRCEECPPGY	33 (SEQ ID NO: 188)

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Please replace Table 10E on page 116 with the following:

Table 10G Domain Analysis of NOV10			
gnl Smart smart00409, IG, Immunoglobulin			
CD-Length = 86 residues, 89.5% aligned Score = 37.0 bits (84), Expect = 0.001			
Query:	27	SNVTLECNFDTGSHVNLGAITVSLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVR	86
		+VTL C TV+ K R ++ G ++ I V	
Sbjct:	10	ESVTLSCASGNPPP-----TVTWKQGGKLLAESGRFSVSRSG---GNSTLTISNVTPE	61
Query:	87	DEGQYQCIIYGVAWDYKYLTLKVK	111
		D G Y C TL V	
Sbjct:	62	DSGTYTCAATNSSGSASSGTTLTVL	86 (SEQ ID NO: 189)

Please replace Table 11E on page 123 with the following:

Table 11E. Domain Analysis of NOV11			
gnl Smart smart00406, IGv, Immunoglobulin V-Type			
CD-Length = 80 residues, 96.2% aligned Score = 34.7 bits (78), Expect = 0.008			
Query:	52	VELQCQLFPNISAEDMELRWYRCQPSLAVHMERGMMDGGEQKWQYRGRTTFMSDHVARG	111
		V L C+ + + W R P + + Y+GR T D+ ++	
Sbjct:	2	VTLSCKASGF-TFSSYYVSWVRQPPGKGLEWLGYIGSDVSYSEASYKGRVTISKDN-SKN	59
Query:	112	KAMVRSHRVTTFDNRTYCC	130
		+ + D TY C	
Sbjct:	60	DVSLTISNLRVEDTGTYYC	78 (SEQ ID NO: 190)

Please insert the sequence listing pages 1-198 at the end of the specification.

REMARKS

In response to the March 27, 2002 Notice to File Missing Parts of Nonprovisional Application, Applicants submit herewith a computer readable form (CFR) copy of the "Sequence Listing"; a paper copy of the "Sequence Listing"; and a statement that the content of the paper and computer readable copies are the same and include no new matter, in